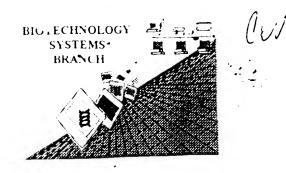
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/701,947
Source:	PCT
Date Processed by STIC:	09/05/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 c-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 c-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

Checker Version 3.0

The Checker Version 3 0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3 0 works for sequence listings generated for the original version of 37 CFR §§1 821 – 1 825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25

Checker Version 3 0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

	 	
RROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 4/20/947	
TTN: NEW RULES CASES	: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAR	₹E
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use apace characters, instead.	
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6PatentIn 2.0 "bug"	A "bug" in Patentln version 2.0 has caused fire <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
,	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.	
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.	
,	In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
0Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
1Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
2PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
3Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa

PCT09

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DATE: + * 11.1
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                       FATENT AFFILMATION: US/09/701,947 TIME: 1:F:
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                        rat Set: N:\CRF3\09052001\I701947.raw
        3 - 110- Applicant: Univergity of Georgia Redearch Froncation, 100.
        5 K120% TITLE OF INVENTION: STABILIZED BY ADDIVE REFTILES AND METHOD OF
                IDENTIFICATION, SYNTHESIS AND COM
        $ <130 - File Reference: 136.0201.13
TC--> 10 <140> CURRENT APPLICATION NUMBER: US/09/701,947
 C--> 11 <141> CURRENT FILING DATE: 2000-12-05
       13 (15) - FRIOR APPLICATION NUMBER: 68 (104,013
       14 <151% FRIOR FILING DATE: 1998-10-13
       16 k150 FRIOR APPLICATION NUMBER: 60 111,18
                                                                     : 1 = E
       17 <151 - FRIOR FILING DATE: 1998-12-14
       19 (16): NUMBER OF REQ ID NOS: 110
       22 <1700 SCFTWARE: Fatentin Ver. 2.0
       25 KUIDH SEQ ID NO: 1
         :::11: LENGTH: 133
       27
       29 HILL TYPE: DNA
       31 MM37 ORGANISM: Escherichia coli
       35 44000 SEQUENCE: 1
       37 qqdagtqago qoaacgcaat taatgtgagt tagctrartr attaggcaco roaggcatta bu
       39. pactitatgo tippuyotby taiyitgidi xqaatiutga qoggataaca atticacaca 120
       41 qqaaaraget atg
       45 (U1): SEQ ID NO: 2
                                                    Unknowns in a sequence listing must be incomerated in fields 221, 222, and
                                          Gricel
         4011: LENGTH: 25
       49 KUllin TYPE: PRT
                                                    223 as well as 18 ted in the siquence
       51 <2130 ORGANISM: Artificial Sequence
       55 <1200 FEATURE:
                                                     Inting.
       57 <223: CTHER INFORMATION: Description of Artifical al Sequence: peptide
               naving opposite charge ending motif
       #3 <4000 SEQUENCE: 2
   60
  W--> 71  Xaa Xaa Xaa Xaa Xaa Arg Lys Arg Lys
                        2.0
       79 - 21). SEQ II NO:
         211 LENGTH: 14
       ra - 212 - TYPE: FAT
       85 K213 - ORGANISM: Artificial dequence
       89 - 228 - FEATTRE:
       91 - 223 - CTHEF INFOFMATION: Lescription of Artificial Coquence: starificed
               angitteman
       97 +400 → ŚEŚTENCE: 3
       49 Fro Exo Aug Ard Val Tyr Ile His Ero Ene Hus Ile Ero Er
       177 - 21% - JEZ 11 11 : 4
       119 - 211 - LENGTH: 1x
       111 - 112 - TYEE: FET
                                                                Use of n and / or Xaa has been detected in the
       113 × 213 × SFRANISM: Artiferral Cequency
                                                                Sequence Listing. Review the Sequence Listing
       11" ×201× FEATMRE:
                                                                to ensure a corresponding explanation is present
                                                                in the <220> to <223> fields of each sequence
                                                               using n or Xaa
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RAW SEQUENCE LISTING

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128 + 4.7 + 08,7781178: 4
    "Mu Aug Mu Asp Asp Ard Val Dyn Lled How Fro Fred How Lee Ard Dyn
133 Arg Lys
141 %210% SE; ID N : 8
143 2114 LENSTH: 1
    2125 TYPE: EFT

«213° CBGANIUM: Home sapiens

151 -400> SEÇMENME: 5
    Asp Arg Val Tyr II+ His Fr. in- His i.-
101 2102 LEÇ II NA: 6
163 - 211> LENGTH: L
165 *212 TYPE: NYA
167 - 2135 ORGANIUM: Artificial Mequence
171 - 220> FEATURE:
173 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
177 k400> SEQUENCE: 6
179 gttgocattg atgcaggoat
183 t21(> SEQ ID No:
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189 - 213 - CRGANION: Artificial Pequence
193 LIBCA FEATURE:
195 (123) OTHER INFORMATION: Description of Artificial Jequence: primer
199 <400> SEQUENCE: "
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                                                                       1 4
107 <211~ LENGTH: 3
209 212% TYPE: DNA
211 4213 > CRGANISM: Artificial Sequence
215 <2200 FEATURE:
117 /223 OTHER INFORMATION: Description of Ambilidial despense: primer
221 +400 - JEQUENCF: -
    attgaattsa matygasan sättyvätty tyhiikk
    -110 SEQ 11 14: 9
    LII - LENGTH: I +
AŠ1 PL12 TYPE: DIA
E31 L13 ORGANISM: Artificial despuence
4:3
    L25 · FEATURE:
gas, 123% OTHER INFORMATION: loweright in it Artificities in quantity from
243 :4000 SEQUENCE: *
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1211 - LENGTH: 4:
LEB - 212 - TYPE: DNA
NET - 213 - NEWMINE ARTICLEAU Geganne
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295 ×211 × LENGTH: 11	
297 42124 TYPE: CNA	
299 × 213 + ORGANION: Astificial deguence	
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309 ×4000 3EQUENCE: 10	
311 tacataaage ttygoctgog ogyttattat tarntt	0
318 k210% 3EQ ID NO: 13	
317 ×211× LENGTH: 4	
319 ×2120 TYPE: 10A	
321 ×213× ORGANIUM: Antificial Sequence	
125 (220) FEATTRE:	
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H2T K223 - OTHER INFORMATION: lescription of Art. Field N-pa-model prime. 331 <400 - SEQUENCE: 13	
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331 <400	47 8
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331 *400 * SEQUENCE: 13 333 tatcatotic adaggaaaca gotatgacca tijanticing ticactig 537 *210 SEQ ID No: 14 739 *211 * LENGTH: 4' 341 *212 TYPE: CNA 345 *213 * ORGANIOM: Artificial Sequence 747 *220 * FEATURE: 349 *223 * OTHER INFORMATION: Lescription : Artificial Sequence: promess 3400 * SEQUENCE: 14 355 * tacatactor: arradigaaa; notigonigo acquintanta transist 359 *410 * SEL ID No: 15 361 *211 * LENGTH: 4'' 763 *212 TYPE: CNA 765 *213 * ORGANIOM: Artificial Sequence 360 *213 * ORGANIOM: Artificial Sequence 361 *211 * SEL TYPE: CNA 762 *213 * OTHER INFORMATIOM: Description of Artificial Sequence: prove 261 *211 * SEL TERME: 15 371 * Satisfagat Sequence: 15 371 * Satisfagat Sequence: 16 371 * Satisfagat Sequence: 17	47 8
331 *400* SEQUENCE: 13 333 tatcatctgc abaggaaaca gotatgacca tgattacdga ttcactg 337 *210 SEQ ID No: 14 339 *211* LENGTH: 4" 341 *212* TYPE: DNA 345 *213* ARSANIOM: Artificial Sequence 247 *220* FEATURE: 349 *123* OTHER INFORMATION: Lescription : Artificial Sequence: prime 353 *400* SEQUENCE: 14 355 taccatactd: arraggaaa; httggorg: wordtratta trattt 359 *410* SEQ II in: 15 361 *211* LENGTH: 4" 363 *213* DREADIOM: Artificial degree e 364 *213* DREADIOM: Artificial degree e 365 *213* DREADIOM: Artificial degree e 367 *214* DREADIOM: Artificial degree e 368 *215* DREADIOM: Artificial degree e 369 *210* DREADIOM: Artificial degree e 360 *211* LENGTHE: 370 *410* SEQUENCE: II 371 *410* SEQUENCE: II 372 *410* SEQUENCE: II 373 *410* SEQUENCE: II 374 *410* SEQUENCE: II 375 *410* SEQUENCE: II 377 *410* SEQUENCE: II 378 *4210* SEQUENCE: II 379 *4210* SEQUENCE: II 370 *4210* SEQUENCE: II 371 *4210* SEQUENCE: II 371 *4210* SEQUENCE: II 372 *4210* SEQUENCE: II 373 *4210* SEQUENCE: II 374 *4210* SEQUENCE: II 375 *4210* SEQUENCE: II 376 *4210* SEQUENCE: II 377 *42	47 8
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331 *400* SEQUENCE: 13 333 tatcatctgc abaggaaaca gotatgacca tgattacdga ttcactg 337 *210 SEQ ID No: 14 339 *211* LENGTH: 4" 341 *212* TYPE: DNA 345 *213* ARSANIOM: Artificial Sequence 247 *220* FEATURE: 349 *123* OTHER INFORMATION: Lescription : Artificial Sequence: prime 353 *400* SEQUENCE: 14 355 taccatactd: arraggaaa; httggorg: wordtratta trattt 359 *410* SEQ II in: 15 361 *211* LENGTH: 4" 363 *213* DREADIOM: Artificial degree e 364 *213* DREADIOM: Artificial degree e 365 *213* DREADIOM: Artificial degree e 367 *214* DREADIOM: Artificial degree e 368 *215* DREADIOM: Artificial degree e 369 *210* DREADIOM: Artificial degree e 360 *211* LENGTHE: 370 *410* SEQUENCE: II 371 *410* SEQUENCE: II 372 *410* SEQUENCE: II 373 *410* SEQUENCE: II 374 *410* SEQUENCE: II 375 *410* SEQUENCE: II 377 *410* SEQUENCE: II 378 *4210* SEQUENCE: II 379 *4210* SEQUENCE: II 370 *4210* SEQUENCE: II 371 *4210* SEQUENCE: II 371 *4210* SEQUENCE: II 372 *4210* SEQUENCE: II 373 *4210* SEQUENCE: II 374 *4210* SEQUENCE: II 375 *4210* SEQUENCE: II 376 *4210* SEQUENCE: II 377 *42	47 n

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419 ×400% PEQUENCE: 10
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425 -210: SEQ IP De: 15
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          LENGTH: 35
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         TYPE: INA
431 -2150 VRGANIUM: Artificial Sequence
435 ×220: FEATURE:
437 223° OTHER INFORMATION: Lescription i Artificial Degreence: primer
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447 -210> SEQ ID NY: 19
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453 %213% ORGANISM: Artificial Sequence
457 H221H FEATURE:
459 K223 OTHER INFORMATION: Description of Artificial Companies primer
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465 attagtgaat trypacaate tetgrastas ytrit
469 :210» SEQ ID NO: L
471 <2112 LENGTH: 15
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475 <213> @RMANIUM: Artificial Sequence
479 <220≥ FEATURE:
461 /223> OTHER INFORMATION: Testription of Artificial Sequence: primer
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         iraqman:
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RAW SEQUENCE LISTING

TATENT APPLICATION: US/09/701,947